APPENDIX F
Application 10/782,435
Docket 1121C RuvB

GAP comparison of sequences in WO 2004/003013 application.

Polynucleotides – Percent Sequence Identity

SEQ ID	CQ760237	CQ760239	CQ760241
1	72.694	52.193	51.695
3	72.767	52.852	52.119
5	72.767	52.281	51.342
7	72.840	52.535	51.412
9	73.152	50.797	51.133

Polypeptides – Percent Sequence Identity

SEQ ID	CQ760237aa	CQ760239aa	CQ760241aa
2	84.615	45.946	44.965
4	85.055	45.946	44.965
6	85.275	45.270	44.836
8	85.275	45.495	44.836
10	85.388	45.902	45.122

GAP of: CQ760237 check: 1467 from: 1 to: 1377

WPDEF 1121 RuvB NCBI CQ760237 from WO2004/00313
1121 RuvB NCBI CQ760237 from WO2004/00313
LOCUS   CQ760237   1377 bp   DNA   linear   PAT 17-APR-2005
DEFINITION Sequence 4 from Patent WO2004003013.
ACCESSION   CQ760237
VERSION   CQ760237.1 GI:44903794 . . .

 to: 1121SID3 check: 4044 from: 1 to: 1912

WPDEF Case 1121 SEQ ID NO: 3 RuvB

 Symbol comparison table: nwsgapdna.cmp CompCheck: 8760

         Gap Weight: 50   Average Match: 10.000
      Length Weight: 3   Average Mismatch: 0.000

           Quality: 10020   Length: 1912
             Ratio: 7.277   Gaps: 0
Percent Similarity: 72.767   Percent Identity: 72.767

       Match display thresholds for the alignment(s):
                    | = IDENTITY
                    : =   5
                    . =   1

  1121CQ760237 x 1121SID3   October 4, 2005 17:43 ..

                    .   .   .   .   .
     1 ....atggagaaagtaaaga 16
                                        ||| | | | ||
    51 ctccacagaaacagagagcgcataaccggcggcgttggcggcgatgagga 100

           .   .   .   .   .   .
    17 ttgaagaaattcagtccaccgctaagaaacaacggattgctactcacacc 66
        | || || | |||||| ||| | |||||| || || || || || ||||||
   101 tcgaggaggtgcagtcgacctcgaagaagcagcgcatcgccacccacacc 150

           .   .   .   .   .   .
    67 catatcaaaggccttggcctcgagccaactggtatccctataaaattggc 116
        || ||||| || || ||||||||| | | ||| || | || |||||
   151 cacatcaagggactcggcctcgacgccaatgggatggcgattgcgttggc 200

           .   .   .   .   .   .
   117 agctggatttgttggtcaacttgaggctagagaggcagctggtcttgtag 166
        || || || || || || || | ||| | ||||| || || || | |
   201 ggcggggttcgtgggccaggcggcggcgcgcgaggcggccgggctggcgg 250

           .   .   .   .
   167 ttgacatgattaagcagaagaaaatggcgggcaaggctcttttgcttgct 216
        | ||||||||| ||||||||| ||||| ||| || | | ||||||
   251 tcgacatgattcgccagaagaagatggccggccgcgcggtgctccttgcg 300

```
217 ggacctcctggaactgggaaaacagctttggctcttggaatctctcaaga 266
    || || || |  || || || || ||  | || || || ||  | || ||
301 ggtccgcccgccacgggcaagacggcgctagcgctcggcatagcccagga 350

267 gctgggaagcaaggttccattctgtccaatggttggatctgaggtttact 316
    ||| || |||||||||| || ||||||||| ||||| |||||| || || ||||
351 gctcggcagcaaggtccctttctgtcctatggtaggatcagaagtgtact 400

317 catcagaggttaagaaaacagaggttctcatggagaattttagacgtgcc 366
    | || ||||| ||||||||| ||||| || ||||| |||||  |  | ||
401 cctcggaggtcaagaaaactgaggtgctgatggaaaatttccgtagagct 450

367 attggtctacgtatcaaggaaaccaaagaagtctatgaaggggaggtcac 416
    || ||| | ||||| ||||||| ||||||| || |||||||| ||||| ||
451 ataggtttgcgtataaaggaaaacaaagaggtttatgaaggagaggttac 500

417 cgagctgtcaccagaagaaactgaaagcctcactggaggttatggtaaaa 466
    || || || |||||||||  |||| ||      |||||| || ||||  ||||
501 tgaactttccccagaagaggctgagagtacaactggtggatatgcaaaaa 550

467 gcatcagccatgttgtaattacactcaagacagtcaaaggaaccaaacat 516
    |||| |||||||| | || |   | ||||| || ||||| || || ||
551 gcattagccatgtaatcatcagcttaaagactgttaaagggactaagcaa 600

517 ctgaaattggatcccactatctatgatgccttgattaaggaaaaggtagc 566
    |||||  || ||| |  | || ||||||||  |||| ||||||||||| ||
601 ctgaagttagattcttcaatttatgatgctctgatcaaggaaaaggtggc 650

567 tgtaggagatgtaatctatatcgaagcaaacagtggagctgtcaaacggg 616
    || ||  |||||| || || ||||||||||| ||||||||  || ||| | |
651 agtgggtgatgttatatacatcgaagcaaatagtggagcagtgaaaagag 700

617 taggtagaagtgatgcttttgccactgaatttgatctggaagcagaagaa 666
    |  |||||| |||||| ||||||| || |||| |||||| ||||| |||||
701 ttggtagatgtgattcttttgctacagaatacgatcttgaagctgaagag 750

667 tatgttccacttcccaaaggagaggtccacaaaaagaaagagatagtgca 716
    ||||||||  | ||||||||| || ||||| || || ||||| || |||||
751 tatgttcctatccccaaaggtgaagtccataagaaaaaagaaattgtgca 800

717 ggatgtcacactccaagatctggatgcagcaaatgctcgacctcaaggtg 766
    ||||||||||| || || || ||||||||||||||||  || |||||||
801 ggatgtcacacttcatgaccttgatgcagcaaatgctcagccacaaggtg 850

767 gccaggatatactttctttgatgggccaaatgatgaaaccgcggaagact 816
    |||| |||||| | ||  | |||||||||| |||||||||| || ||||||
851 gccaagatattttgtcccttatgggccagatgatgaaaccacgaaagact 900

817 gagatcactgataagcttcggcaagaaattaacaaggttgtgaaccgata 866
    || |||||| || || || || ||||||||||||| ||||| || || ||||
901 gaaatcaccgaaaaactacgccaagaaattaataaggtggtaaatagata 950
```

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 867 tatagatgaaggtgtggcagagcttgttccaggagttctatttattgatg  916
     ||| |||||||||  | ||||||||||| || ||  ||| | || ||||||||
 951 tatcgatgaaggaattgcagagcttgtacctggtgtttttgttcattgatg 1000

 917 aggttcatatgcttgatatggagtgcttctcatacttgaaccgtgctctt  966
     |||| || ||| | ||||| || || || || ||  | ||||||||  |
1001 aggtccacatgttggatatcgaatgttttctcatcttaaccgtgcattg 1050

 967 gagagctcattatctccgatagtgatatttgcaacaaatagaggtgtttg 1016
     ||||||  |||||||  || ||  ||||||  ||||  ||||||||| ||   | ||
1051 gagagcccattatcaccaatcgtgatacttgctacaaataggggaatatg 1100

1017 caacgtaagagggactgatatgcccagcccccatggagtccctattgatc 1066
     || ||||||||| |||||||||| | || || |||||  | ||  | ||||
1101 taatgtaagaggaactgatatgacaagtccacatggtataccggtggatc 1150

1067 tattagatcgattggttatcatccggactcaaatctatgatccctctgaa 1116
     |  ||||| |  |||| || || |||||| | |  ||||  ||  ||||
1151 ttctagataggctggtgattattcggacagagacatatggccctactgag 1200

1117 atgatccagattatagccattcgtgcgcaagttgaagaattaaccgtgga 1166
     ||||| |||||   | || || || || ||||| || ||  |      ||||
1201 atgatacagatattggctatccgagcacaagtggaggagattgatatgga 1250

1167 tgaagaatgcttggttctacttggggagattgggcaaagaacttcactaa 1216
     |||||||  |   | | |       |  || ||||||  || ||     || ||   | |
1251 tgaagaaagtcttgcttatttaggcgagatcggacagcagacatctttga 1300

1217 ggcacgctgtgcagcttctgtctcctgccagcattgtagcgaaaatgaat 1266
     |  ||  ||| |  || |   |  || |||||||||| |  || | ||  |  |||
1301 gacatgctattcaattgatatcacctgccagcgtggtctcaaagactaat 1350

1267 ggccgtgacaatatttgcaaggctgatatagaggaagtaacatcactcta 1316
     ||  | | ||  ||  || ||||||||||||| | ||||||||| |      |||||
1351 ggaagagagaaaatctgcaaggctgatctcgaggaagtcagtgggctcta 1400

1317 cttggatgctaaatcttcagcaaagcttttgcatgagcaacaagaaaaat 1366
     ||||||||  ||||| || ||    ||| | || ||||||||||||||| ||
1401 tttggatgccaaatcctcggctcggctgctccaggagcaacaagaaagat 1450

1367 acatctcatga...................................... 1377
     |||||  | |
1451 acatcacctagatttggatctcctgtcgtggaagtctcgaagagaatgta 1500
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GAP of: CQ760237aa   check: 5361   from: 1   to: 458

WPDEF 1121 RuvB NCBI encoded by CQ760237 from WO2004/00313
1121 RuvB NCBI encoded by CQ760237 from WO2004/00313
SEQ ID NO: 5 NCBI CAF32893 .
LOCUS   CQ760237   1377 bp   DNA   linear   PAT 17-APR-2005
DEFINITION Sequence 4 from Patent WO2004003013.
ACCESSION   CQ760237 . . .

to: 1121SID4   check: 8436   from: 1   to: 455

WPDEF Case 1121 SEQ ID NO: 4 RuvB

Symbol comparison table: blosum62.cmp CompCheck: 1102
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
           substitution matrices from protein blocks. Proc. Natl.
Acad.
        Sci. USA 89: 10915-10919.

          Gap Weight: 8   Average Match: 2.778
       Length Weight: 2   Average Mismatch: -2.248

            Quality: 1994   Length: 458
              Ratio: 4.382   Gaps: 0
  Percent Similarity: 90.110   Percent Identity: 85.055

        Match display thresholds for the alignment(s):
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                    : =   2
                    . =   1

1121CQ760237aa x 1121SID4 October 4, 2005 18:01 ..

  1 MEKVKIEEIQSTAKKQRIATHTHIKGLGLEPTGIPIKLAAGFVGQLEARE 50
      .:|||:|||.|||||||||||||||: |. | |||||||| |||
  1 ...MRIEEVQSTSKKQRIATHTHIKGLGLDANGMAIALAAGFVGQAAARE 47

 51 AAGLVVDMIKQKKMAGKALLLAGPPGTGKTALALGISQELGSKVPFCPMV 100
    |||| ||||:|||||||:|.|||||| |||||||||||.||||||||||||
 48 AAGLAVDMIRQKKMAGRAVLLAGPPATGKTALALGIAQELGSKVPFCPMV 97

101 GSEVYSSEVKKTEVLMENFRRAIGLRIKETKEVYEGEVTELSPEETESLT 150
    |||||||||||||||||||||||||||||| |||||||||||||| || |
 98 GSEVYSSEVKKTEVLMENFRRAIGLRIKENKEVYEGEVTELSPEEAESTT 147

151 GGYGKSISHVVITLKTVKGTKHLKLDPTIYDALIKEKVAVGDVIYIEANS 200
    ||| ||||||:|.|||||||| |||| .|||||||||||||||||||||||
148 GGYAKSISHVIISLKTVKGTKQLKLDSSIYDALIKEKVAVGDVIYIEANS 197

```
201 GAVKRVGRSDAFATEFDLEAEEYVPLPKGEVHKKKEIVQDVTLQDLDAAN 250
    |||||||| |·||||:|||||||||:||||||||||||||||| ||||||
198 GAVKRVGRCDSFATEYDLEAEEYVPIPKGEVHKKKEIVQDVTLHDLDAAN 247

251 ARPQGGQDILSLMGQMMKPRKTEITDKLRQEINKVVNRYIDEGVAELVPG 300
    |·||||||||||||||||||||||||:|||||||||||||||:||||||
248 AQPQGGQDILSLMGQMMKPRKTEITEKLRQEINKVVNRYIDEGIAELVPG 297

301 VLFIDEVHMLDMECFSYLNRALESSLSPIVIFATNRGVCNVRGTDMPSPH 350
    |||||||||||·|||||||||||| |||||| |||||:||||||||| |||
298 VLFIDEVHMLDIECFSYLNRALESPLSPIVILATNRGICNVRGTDMTSPH 347

351 GVPIDLLDRLVIIRTQIYDPSEMIQIIAIRAQVEELTVDEECLVLLGEIG 400
    |:|:|||||||||||: | |·|||||:||||||||: ·||| |  |||||
348 GIPVDLLDRLVIIRTETYGPTEMIQILAIRAQVEEIDMDEESLAYLGEIG 397

401 QRTSLRHAVQLLSPASIVAKMNGRDNICKADIEEVTSLYLDAKSSAKLLH 450
    |·||||||:||:||||:|·| |||: |||||:|||· ||||||||:||
398 QQTSLRHAIQLISPASVVSKTNGREKICKADLEEVSGLYLDAKSSARLLQ 447

451 EQQEKYIS 458
    ||||:||·
448 EQQERYIT 455
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